05-11529 NG

To: Denise Regan
From: Yue Zheng
Date: December 5, 2005

Re: The admissibility of the DNA evidence

a. The DNA evidence is exculpatory

If Mr. Grinkley's body came into contact with Chantel's, it would most likely have left at least a few of its some 100 trillion cells behind. As Dr. Riley stated in his report, each human cell has all of the genetic loci that were tested. So, if the sample had cells from Michael Grinkley in it, there would be positive results for all his alleles. Yet, six of the defendant's genetic markers (alleles) are missing from Item 5b, a perianal swab from Chantel and the only sample that showed any sign of DNA not belonging to Chantel. Therefore, Item 5b does not contain Michael Grinkley's DNA, suggesting that his body did not come into contact with Chantel's.

Now, there are 4 alleles in the sample foreign to Chantel which Mr. Grinkley happens to have. It would be illogical to conclude that these alleles came from Michael Grinkley because 6 of his alleles are missing from the sample. A person cannot deposit some of his DNA and not the rest because each tiny cell contains all of his DNA. There is no literature supporting the theory of a person depositing "half a cell."

Well, where did these 4 foreign alleles come from? Dr. Riley has stated that these alleles are common in the general public and even more common in a family setting. The most straightforward explanation is that another person deposited these alleles, someone who possesses these 4 alleles and has all the same alleles as Chantel in the other loci. Someone who has that high a degree of genetic similarity to Chantel would almost have to be a family member. So far, only Michael Grinkley has been tested. Without

conducting DNA tests on the rest of the family, it would be impossible to find the true donor of these 4 alleles.

For the foregoing reasons, these test results are actually exculpatory.

b. The unfair prejudice and confusion the test results will cause far outweigh the probative value.

Despite the exculpatory value of the DNA results, the nature of DNA evidence is complex and thus confusing, and there is an enormous risk that jurors may overweigh the positive results on the 4 alleles. Regarding the confusing nature of this evidence, the complex charts, technical vocabulary, and the analysts' own statements that the test results are inconclusive speak for themselves. The honest truth is that even lawyers' and judges' eyes often "glaze over" upon seeing these data.

As to the risk of unfair prejudice, Ms. Joseph has already coined the term "partial match" for the results on Item 5b because of the positive results for 4 alleles. "Partial match" is an unfair and erroneous characterization of these results. For the term "partial match" to be accurate, the 4 "matching" alleles would actually have to have come from the defendant into the sample while the rest of his DNA, his other alleles, magically stayed out. As discussed above, each cell has all of a person's DNA and no literature supports the theory of depositing "half a cell." Cells are so tiny they are invisible to the unaided eye. They do not come apart or get smudged like a fingerprint. Even if one cell broke apart and its DNA got severed and only some pieces fell onto Chantel, many more of a body's some 100 trillion cells would have fallen as whole cells. The whole cells would have all of the person's DNA. Very simply, six of the defendant's alleles were absent from the DNA test results, and therefore, that DNA did not come from the defendant.

Nevertheless, when a jury, already confused by the technical jargon and quantitative data, considers the positive results for the 4 alleles, they may well adopt the "partial match" idea. On the surface, "partial match" may sound right. A juror may find everything else confusing, but the idea that since some of the sample's numbers do not match up with the defendant's and some of the numbers do, all of the data can be considered a "partial match" may be the only thing that sounds clear.

One would have to ignore all of the above information to actually accept the idea of "partial match" as true. Yet, many will admit that they often find scientific details to be over their heads. There is a reason why forensic science, molecular biology and the study of DNA are specialized fields. Therefore, the risk of the jury becoming confused and overweighing the positive results for the 4 alleles far outweighs the probative and indeed exculpatory value of the DNA evidence. As such, the DNA test results must be excluded.

CONCLUSIONS

Kishawra Barrett-Pearson is included as being the possible source of the DNA extracted from Item 4b Anorectral Swab #1A. This combination of DNA "types", or genotypes, could be expected to be found in approximately 1 in 7.7×10^{17} Caucasians, 1 in 5.3×10^{17} African Americans, and 1 in 1.3×10^{18} Southeastern Hispanics.

The DNA extracted from Item 5b Perianal Swab #1A is consistent with being a mixture of DNA from two or more individuals. Chantel Barrett-Pearson is included as being a possible contributor to the mixture. Michael Grinkley cannot be included or excluded as being a possible contributor to the mixture. A complete DNA profile consistent with Michael Grinkley was not detected. However, no alleles were detected that could not have come from Chantel Barrett-Pearson and Michael Grinkley. Approximately 1 in 1.8×10^{11} Caucasians, 1 in 3.2×10^{11} African Americans, and 1 in 1.6×10^{11} Southeastern Hispanics are included as being possible contributors to the mixture.

Chantel Barrett-Pearson is included as being the possible source of the DNA extracted from Item 5b Genital Swab #1A. This combination of DNA "types", or genotypes, could be expected to be found in approximately 1 in 1.3×10^{17} Caucasians, 1 in 7.6×10^{16} African Americans, and 1 in 1.4×10^{17} Southeastern Hispanics.

Note: Allele frequencies for markers D2S1338 and D19S433 are not included in combined genotype frequency calculations.

DISPOSITION OF EVIDENCE

DNA extracts are kept for a period of 3 years; a portion of the original sample is retained for any additional testing.

Please contact me if you have any questions regarding the DNA analysis performed on this case.

Respectfully submitted,

Julie K Lynch

Julie K. Lynch

Reviewed by,

Joseph Varlaro

Joseph Varlaro

Commonwealth v. Michael Grinkley

Scientific report of Donald E. Riley, Ph.D.

Introduction.
I am a research scientist, trained as a biochemist and molecular biologist. I have post-doctoral training in molecular biology and genetics. I have 28 years of professional experience performing and publishing original scientific research involving DNA technology.

A crucial part of the scientific process is independent scientific review. In research, this is done by anonymous reviewers who determine the majority of publication and funding decisions. Anonymity helps ensure that reviewers may comment stringently and freely. Criticism and critical review are important, integral parts of graduate level training and research in the biological sciences. Most scientists I am familiar with are highly trained as critical reviewers and also have their work regularly critiqued by others.

The National Research Counsel (NRC) of 1992 stated:

> *"The same standards and peer-review processes used to evaluate advances in biomedical science and technology should be used to evaluate forensic DNA methods and techniques."*

I am familiar with the forensic DNA literature. I have authored original publications involving various short tandem repeats (STRs) including many identical to STRs used in the instant case. STRs are short, repeating DNA structures that form the basis for currently popular, forensic DNA tests. I have consulted in approximately 210 forensic DNA cases.

I have written a popular article entitled, "DNA Testing, an Introduction for Non-scientists." The article has been requested as distribution material at multiple legal meetings and symposia including, *The Women's Bar Association of the State of New York* and *The National Reference Center for Bioethics Literature.* Among approximately 64 anonymously peer-reviewed, scientific articles that I have written, or co-authored, 43 articles deal specifically with DNA, 20 involve the polymerase chain reaction (PCR) and nine involve STRs.[1] In recent research, I discovered independent lines of evidence that some STRs function, findings that tend to revise understanding of STRs. This recent work was reviewed and approved by multiple, anonymous scientists and known editors at three, independent, scientific journals.

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[1]PCR is a technique used to copy small amounts of DNA. The process can lead to dramatic increases in the amount of DNA available, but the process has important limitations. PCR, using reagents from the commercially supplied DNA testing kit, Identifiler™ (PE Applied Biosystems, Foster City, CA) was used as the DNA typing system in the instant case.

The DNA testing laboratory and perspective.

I have previously visited and witnessed testing at the Boston Police Crime Laboratory. The DNA analysts there have been capable, serious professionals. Currently, most differences among professionals arise when samples are minimal, mixed or otherwise challenging as in this case.

The instant case.

I was hired by defense counsel, Denise Regan, to review scientific materials in the instant case. I reviewed laboratory reports, notes, electropherogram tracings, protocols and a Quantiblot image.

Laboratory notes and records indicated that a variety of items were examined using a presumptive test for semen with negative results. These items included items of clothing, genital swabs, perianal swabs and oral swabs. The oral, vaginal and anal swabs were also examined for intact sperm with negative findings. The DNA laboratory chose a DNA extraction method that doesn't attempt to segregate sperm and non-sperm cells. Presumably this extraction method was chosen because no sperm were found. The choice of extraction methods was reasonable, but it should be kept in mind that the organic extraction method used will extract DNA from most human cell types including epithelial cells, white blood cells and many other cell types.

The Boston Police Crime Laboratory Report of March 9, 2004 stated:

"The DNA extracted from Item 5b Perianal Swab #1A is consistent with being a mixture of DNA from two or more individuals. Chantel Barrett-Pearson is included as being a possible contributor to the mixture. Michael Grinkley cannot be included or excluded as being a possible contributor to the mixture. A complete DNA profile consistent with Michael Grinkley was not detected. However, no alleles were detected that could not have come from Chantel Barrett-Pearson and Michael Grinkley."

This statement that Michael Grinkley cannot be included or excluded is very unusual. I don't recall seeing such a statement previously since individuals are normally said to be included, excluded, or the results inconclusive.

Inspection of the data revealed that, as the DNA laboratory stated, a complete DNA profile consistent with Michael Grinkley was not detected. The statement that the defendant could not be excluded seemed to suggest the laboratory suspects there may be a partial profile consistent with Mr. Grinkley. However, I see no compelling reason to make that suggestion. In fact, the defendant has six genetic markers (alleles) that were absent from Item 5b Perianal Swab #1A according to my reading of the data. Each human cell has all of the genetic loci that were tested. So, the results do not reflect the equivalent of even one human cell consistent with Mr. Grinkley. The report did not state and perhaps did not consider that, while Item 5b #1A has some alleles different from those of the alleged victim, they may be from a source other than Mr. Grinkley.

Absence of even one or two genetic markers forms an exclusion unless one is interpreting the results in a way that assumes that "missing" parts of a profile are due to test or sample failures at those sites. Any such assumption precludes use of the putative profile because the assumption is one of unreliability. Again, human cells do not have partial profiles. If a partial profile is asserted, then the laboratory must come to grips with system or sample insufficiency.

The laboratory went on to state that "Approximately 1 in 1.8×10^{11} Caucasians, 1 in 3.2×10^{11} African Americans, and 1 in 1.6×10^{11} Southeastern Hispanics are included as being possible contributors to the mixture." Presentation of these frequencies, in this context, may be extremely misleading for multiple reasons:

1. The defendant could not be included. To the best of my knowledge, many, if not most, would say he is excluded.

2. Even under a theory that the sample or the test system were unreliable at some loci, there is no way to determine in full, which loci were unreliable.

3. Profile inconsistencies comparing Item 5b Perianal Swab #1A with Mr. Grinkley are not easily explained by degradation, one of the common causes of allele and locus dropout.

4. Alleles that were foreign to the alleged victim would be more common in a family setting than among the population at large. The "match probabilities" in question are usually stated in terms of randomly selected individuals in a population. The alleles consistent with the defendant are not rare among populations and would be much less rare among members of his family.

5. The minor contributor's DNA is likely to be substantially below manufacturer's recommendations for input DNA. Such minimal samples are at increased risk of representing contamination.

Table 1 lists alleles present in the defendant's profile and their status and being absent, unconfirmable due to masking[2], or potentially present in the perianal swab.

Table 1. Comparison of Defendant's profile with Item 5b #1A

Locus	Allele 1	Allele 2
Amelogenin	Small Y peak below reporting threshold[3]	X, doesn't distinguish male/female
D5S818	Homozygous 12 allele unconfirmable	

[2] Masking occurs because there is no way to determine whether a minor component is present at sites that exhibit alleles from a major contributor.

[3] Exact peak heights were not provided although both GeneScan and electronic data were requested. The statement, "below reporting threshold" is based on absence of an allele size in Genotyper printouts.

	(masking effects).	
FGA	21 allele unconfirmable (masking effects).	**Defendant's 24 allele absent (mid mw[4])**
D19S433	Possible 15 allele below threshold.	Possible 15.2 allele below threshold
VWA	17 allele unconfirmable (masking effects).	Possible 19 allele, very small peak below threshold
TPOX	8 allele, small peak above threshold	11 allele unconfirmable (masking effects).
D18S51	16 allele unconfirmable (masking effects)	**Defendant's 19 allele absent (hmw)**
D3S1358	15 allele unconfirmable (masking effects)	16 allele unconfirmable (masking effects)
THO1	6 allele, small peak above threshold	9 allele, small peak below threshold but consistent with stutter (check difficult because peak heights not provided)
D13S317	Possible 11 allele below threshold	12 allele, small peak but consistent with stutter artifact
D16S539	Defendant's 11 allele absent; stutter peak appears here. (peak heights not provided)	12 allele unconfirmable (masking effects).
D2S1338	**Defendant's 19 allele absent (hmw)**	Possible 24 allele, small peak below threshold and consistent with stutter (check difficult due to lack of e-data)
D8S1179	14 allele unconfirmable (masking effects)	15 allele, small peak apparently above threshold
D21S11	**Defendant's 30.2 absent (low to mid mw)**	31 allele unconfirmable (masking effects)
D7S820	Homozygous 8 unconfirmable (masking effects)	
CSF1PO	**Defendant's 8 allele absent (hmw)**	10 allele, small peak below threshold consistent with stutter from large 11 allele

Comparison summary: The defendant's known profile consists of 28 alleles. For Item 5b, perianal swab #1A, there were only 3 clearly reportable, unmasked alleles consistent with Mr. Grinkley and these were common in the total population. They would be even more common within a family setting consisting of Mr. Grinkley's relatives. Two

[4] mw, molecular weight; hmw, high molecular weight.

additional alleles appeared at stutter positions and can't be confirmed without the requested GeneScan data. One of these seems doubtful. There were 8 possible alleles/artifacts below reporting threshold. To their credit, these were not reported by the BPD laboratory, nor should they be reported as being significant. Such signals are at risk of representing artifacts or contaminants. There were 11 alleles in Mr. Grinkley's profile that would not have been detected (unconfirmable) due to allele masking. At least 6 alleles in Mr. Grinkley's profile were absent from Item 5b #1A. If the test system performed reliably and the sample were adequate, one absent allele would constitute an exclusion. Among his two homozygous loci (D5 and D7) neither produced significantly increased peak height in Item 5b, perianal swab #1A. In other words, I see no convincing evidence they were present. Common processes such as DNA degradation do not easily explain the differences comparing Mr. Grinkley's profile with that of Item 5b, perianal swab #1A.

To the best of my knowledge and by normal standards, Mr. Grinkley is excluded as a contributor to Item 5b, perianal swab #1A. The forensic literature does not support interpretations of minor contributors to mixtures combined with simultaneous assumptions about partial profiles. With all due respect, the stated conclusions and random match probabilities seem likely to mislead.

Respectfully submitted,

Donald E Riley, Ph.D. 11-30-05

Donald E. Riley, Ph.D.